

IN THE SPECIFICATION:

Please replace the paragraph beginning on Page 13, line 26 and ending on Page 13, line 33, with the following:

B

The nucleotide sequence of 5610 bp genomic DNA adjacent to the RB was determined, and the obtained nucleotide sequence was analyzed by the GENSCAN algorithm, as developed by Chris Burge in the research group of Samuel Karlin, Department of Mathematics, Stanford University. (~~http://CCR-~~
~~081.mit.edu/GENSCAN.html~~) to predict the presence of a gene. The GENSCAN program and the model that underlies it are described in Burge et al, "Prediction of complete gene structures in human genomic DNA," *J. Mol. Biol.* **268**, 78-94 (1997). As a result, it was found that the transcription of the gene which is closest to RB is initiated from a nucleotide at position 882 from RB, and the gene was designated MSH.